

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/715,035

DATE: 07/17/2001

TIME: 09:36:26

Input Set : A:\Mockel-5.ST25.txt

Output Set: N:\CRF3\07172001\I715035.raw

ENTERED

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5 <110> APPLICANT: Mockel, Bettina
7   Pfefferle, Walter
11 <120> TITLE OF INVENTION: Novel Nucleotide Sequences Encoding the pfkA Gene
15 <130> FILE REFERENCE: 21123/274441
19 <140> CURRENT APPLICATION NUMBER: 09/715,035
21 <141> CURRENT FILING DATE: 2000-11-20
25 <160> NUMBER OF SEQ ID NOS: 4
29 <170> SOFTWARE: PatentIn version 3.0
33 <210> SEQ ID NO: 1
35 <211> LENGTH: 1274
37 <212> TYPE: DNA
39 <213> ORGANISM: Corynebacterium glutamicum
43 <220> FEATURE:
45 <221> NAME/KEY: CDS
47 <222> LOCATION: (143)..(1171)
51 <400> SEQUENCE: 1
52 gtcgatttgt taatgaaact gcagctctgg cgattaaata agatggtcag agacagtttt      60
54 ttggcctgtc aaccctgtg attctcttat ttttgggtga ttgttccggc gcgggtgttg      120
56 tgatgggttt aatatggaag ac atg cga att gct act ctc acg tca ggc ggc      172
57           Met Arg Ile Ala Thr Leu Thr Ser Gly Gly
58           1               5               10
60 gac tgc ccc gga cta aac gcc gtc atc cga gga atc gtc cgc aca gcc      220
61 Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala
62           15               20               25
64 agc aat gaa ttt ggc tcc acc gtc gtt ggt tat caa gac ggt tgg gaa      268
65 Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu
66           30               35               40
68 gga ctg tta ggc gat cgt cgc gta cag ctg tat gac gat gaa gat att      316
69 Gly Leu Leu Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile
70           45               50               55
72 gac cga atc ctc ctt cga ggc ggc acc att ttg ggc act ggt cgc ctc      364
73 Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu
74           60               65               70
76 cat ccg gac aag ttt aag gcc gga att gat cag att aag gcc aac tta      412
77 His Pro Asp Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu
78 75           80               85               90
80 gaa gac gcc ggc atc gat gcc ctt atc cca atc ggt ggc gaa gga acc      460
81 Glu Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr
82           95               100              105
84 ctg aag ggt gcc aag tgg ctg tct gat aac ggt atc cct gtt gtc ggt      508
85 Leu Lys Gly Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly
86           110              115              120
88 gtc cca aag acc att gac aat gac gtg aat ggc act gac ttc acc ttc      556
89 Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe
90           125              130              135
92 ggt ttc gat act gct gtg gca gtg gct acc gac gct gtt gac cgc ctg      604
93 Gly Phe Asp Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu

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94      140      145      150
96 cac acc acc gct gaa tct cac aac cgt gtg atg atc gtg gag gtc atg      652
97 His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met
98 155      160      165      170
100 ggc cgc cac gtg ggt tgg att gct ctg cac gca ggt atg gcc ggc ggt      700
101 Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly
102      175      180      185
104 gct cac tac acc gtt att cca gaa gta cct ttc gat att gca gag atc      748
105 Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile
106      190      195      200
108 tgc aag gcg atg gaa cgt cgc ttc cag atg ggc gag aag tac ggc att      796
109 Cys Lys Ala Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile
110      205      210      215
112 atc gtc gtt gcg gaa ggt gcg ttg cca cgc gaa ggc acc atg gag ctt      844
113 Ile Val Val Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu
114      220      225      230
116 cgt gaa ggc cac att gac cag ttc ggt cac aag acc ttc acg gga att      892
117 Arg Glu Gly His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile
118 235      240      245      250
120 gga cag cag atc gct gat gag atc cac gtg cgc ctc ggc cac gat gtt      940
121 Gly Gln Gln Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val
122      255      260      265
124 cgt acg acc gtt ctt ggc cac att caa cgt ggt gga acc cca act gct      988
125 Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala
126      270      275      280
128 ttc gac cgt gtt ctg gcc act cgt tat ggt gtt cgt gca gct cgt gcg      1036
129 Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala
130      285      290      295
132 tgc cat gag gga agc ttt gac aag gtt gtt gct ttg aag ggt gag agc      1084
133 Cys His Glu Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser
134      300      305      310
136 att gag atg atc acc ttt gaa gaa gca gtc gga acc ttg aag gaa gtt      1132
137 Ile Glu Met Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val
138 315      320      325      330
140 cca ttc gaa cgc tgg gtt act gcc cag gca atg ttt gga tagtttttcg      1181
141 Pro Phe Glu Arg Trp Val Thr Ala Gln Ala Met Phe Gly
142      335      340
144 ggctttttatc aacagccaat aacagctctt tcgccattg aggtggaggg gctgtttttt      1241
146 catgccgtaa ggaaagtga agtaagtga atc      1274
149 <210> SEQ ID NO: 2
151 <211> LENGTH: 343
153 <212> TYPE: PRT
155 <213> ORGANISM: Corynebacterium glutamicum
159 <400> SEQUENCE: 2
161 Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn
162 1      5      10      15
165 Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser
166      20      25      30
169 Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg
```

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170          35          40          45
173 Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg
174          50          55          60
177 Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys
178 65          70          75          80
181 Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp
182          85          90          95
185 Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp
186          100          105          110
189 Leu Ser Asp Asn Gly Ile Pro Val Gly Val Pro Lys Thr Ile Asp
190          115          120          125
193 Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val
194          130          135          140
197 Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser
198 145          150          155          160
201 His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp
202          165          170          175
205 Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile
206          180          185          190
209 Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg
210          195          200          205
213 Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly
214          210          215          220
217 Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp
218 225          230          235          240
221 Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp
222          245          250          255
225 Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly
226          260          265          270
229 His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala
230          275          280          285
233 Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe
234          290          295          300
237 Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe
238 305          310          315          320
241 Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val
242          325          330          335
245 Thr Ala Gln Ala Met Phe Gly
246          340
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249 <210> SEQ ID NO: 3
251 <211> LENGTH: 20
253 <212> TYPE: DNA
255 <213> ORGANISM: PCR primer
259 <400> SEQUENCE: 3
260 aactgcagct ctggcgatta
263 <210> SEQ ID NO: 4
265 <211> LENGTH: 20
267 <212> TYPE: DNA
269 <213> ORGANISM: PCR primer
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273 <400> SEQUENCE: 4

274 aactatccaa acattgcctg

20

VERIFICATION SUMMARY

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